

FIG. 1B

651	TAAGCTCGCT ATTCGAGCGA	CTGTCTCGCC GACAGAGCGG	TCTTTGGCTT AGAAACCGAA	CAAATTTTCT GTTTAAAAGA	GTCTCTCCAT CAGAGAGGTA
701	CTGTGTCTCTG GACACAGGAC	TGTGTTCTTG ACACAAGAAC	GGCTGTCCCT CCGACAGGGA	ATCTTTCTGC TAGAAAGACG	ATTTGTGTGG TAAACACACC
751	TCTCTCTCTT AGAGAGAGAA	CTGCTCTCCT GACGAGAGGA	CTCTGCAGGG GAGACGTCCC	AGCTTCTTTT TCGAAGAAAA	TTCCAACAGT AAGGTTGTCA
801	TTCTCGTTTT AAGAGCAAAA	GTCTCTCTCC CAGAGAGAGG	AGTCTTGAAC TCAGAACTTG	ACTTTTGTCT TGAAAAACAG	CCGAGAGGTC GGCTCTCCAG
851	TCTTTTGTGT AGAAAAACAA	TCCTTGTCTC AGGAACAGAG	TTGGTTCTTT AACCAAGAAA	CTTTGCTTGC GAAACGAACG	TTGCTTGTCT AACGAACGAA
901	GCTTGCTTGT CGAACGAACA	TGTTGAGACA ACAACCTCTGT	GGGTCTCACC CCCAGAGTGG	ATATAGCTCT TATATCGAGA	GGATGGCCTG CCTACCGGAC
951	GAACTTGCTA CTTGAACGAT	TGTAGCCAG ACATCCGGTC	GCTGGCCTCC CGACCGGAGG	AGCTCATAGA TCGAGTATCT	GATCCACTTG CTAGGTGAAC
1001	CCTCCGACTC GGAGGCTGAG	CCAATTTCCC GGTTAAAGGG	CATCTGTCTC GTAGACAGAG	CCTGTGATCC GGACACTAGG	ATATGGGTAT TATACCCATA
1051	GTGTAACCCCT CACATTGGGA	TACTTTGTCT ATGAAACAGA	CATGGAGGTG GTACCTCCAC	ACAATTTTTC TGTTAAAAAG	TCCCTTCAGT AGGGAAGTCA
1101	TTCTTTGTTC AAGAAACAAG	TTACTGACC AAATGACTGG	AGAAAAGTGC TCTTTTCACG	CTACTTGTCC GATGAACAGG	CCTGGTGGCA GGACCACCGT
1151	AGGCCATTCA TCCGGTAAGT	CCTTAGGACC GGAATCCTGG	TTCCCACCAG AAGGGTGGTC	TTCCCTTGTA AAGGAAACAT	GGCAAATCCC CCGTTTAGGG
1201	TCCCCCTTTG AGGGGGAAAC	AGGTCCTTCC TCCAGGAAGG	CTTTCATACC GAAAGTATGG	GCCCTAGGCT CGGGATCCGA	GGTCAATGGA CCAGTTACCT
1251	GAGAGAAAGG CTCTCTTTCC	CAGAAAAACA GTCTTTTGT	TCTTTAAAGA AGAAATTCTT	GTTTTATTG CAAAATAAAC	AGAATAAATT TCTTATTTAA
1301	AATTTTTGTA TTAAAAACAT	AATAAAATGT TTATTTTACA	TTACAATAA AATTGTTATT	AACTAAACTT TTGATTGAA	TTATGAAAAA AATACTTTTT
1351	AA (polyA) TT				

00000000.000001

FIG. 2

	10	20	30	40	50
chf.781	MSQREGSLEDHQ	TDSSISFLPHLEAKIRQ	THNLARLLTKYAEQLLEEYVQ		
		**	***	* * *	
humcntf		MAFTEHSPLTPHRRDLCSRSIWLARKIRSDLTALTESYVK			
		10	20	30	40

	60	70	80	90	100
chf.781	QQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPAL				
	**	*	* *	***	* *
humcntf	HQGLNKNINLDSADGMPVA----	STDQWSELTEAERLQENLQAYRTFHV			
	50	60	70	80	

	110	120	130	140
chf.781	LD-AVRRRQAE LNPRAPRLRSLEDAARQVRALGAAVETVLAALGAAARG			
	*	*	***	* *
humcntf	LARLLEDQQVHFTPTGDFHQAIHTLLQVAAFAYQIEELMILLEYKIPR			
	90	100	110	120

	150	160	170	180	190
chf.781	PGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVP				
		* * *	* *	* *	**
humcntf	NEADGMPINV-----GDGGLFEKKLWGLKVLQELSQWTVRSIHDL-RFIS				
	140	150	160	170	180

200
chf.781 GGVAO

humcntf SHQTGIPARGSHYIANNKKM
190 200

FIG. 3

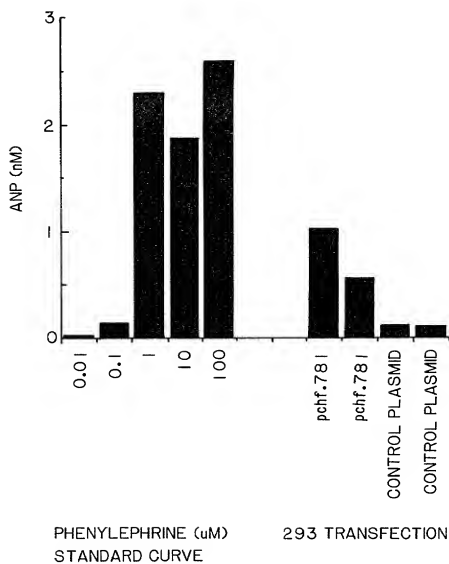
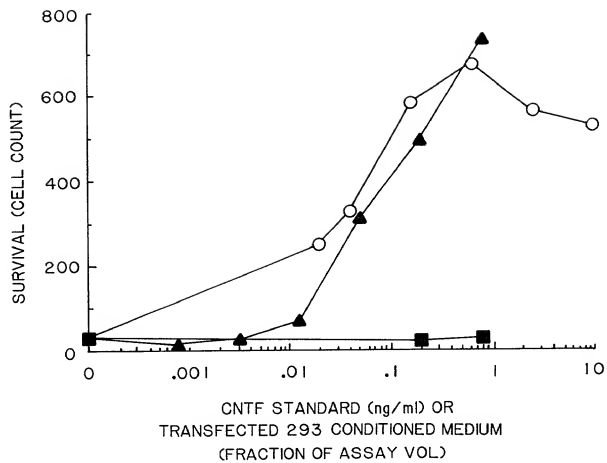


FIG. 4



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humct1      1  MSRRREGSLEDPQTDDSSVLLPHLEAKIRQTHSLAHLTLKYAEQLLQEYVQLQG
                ** ***** **
chf.781     1  MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEVQQQG

humct1      54 DPFGLPSFSPFRLPVAGLSAPASHAGLPVHERLRLDAAALPPLLDVCR
                **** ***** **
chf.781     54 EPFGLPGFSPFRLPLAGLSGAPASHAGLPVSERLRQDAAALSVLPALLDAVRR

humct1      107 RQAE LNPRAPRLRLRLEDAARQARALGAAVEALLAALGAANRGPRAEPPAATA
                ***** **
chf.781     107 RQAE LNPRAPRLRLSLEDAARQVRALGAAVETVLAALGAAARGPGPEPVTAT

humct1      160 --SAASATGVFPKVLGLRVCGLYREWLSRTEGDLGQLLPGSSA
                * * * * *
chf.781     160 LFTANSTAGIFS AKVLGFHVCGLYGEWVSRTEGDLGQLVPGGVA
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